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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/937,215

DATE: 03/05/2002

TIME: 13:58:25

Input Set : A:\1599-0206P.ST25.txt

Output Set: N:\CRF3\03052002\I937215.raw

3 <110> APPLICANT: Lee, Se Yong et al.  
 5 <120> TITLE OF INVENTION: Trehalose Synthase Protein, Gene, Plasmids, Microorganisms,  
 and A Process  
 6 for Producing Trehalose  
 8 <130> FILE REFERENCE: 1599-0206P  
 10 <140> CURRENT APPLICATION NUMBER: US 09/937,215  
 11 <141> CURRENT FILING DATE: 2001-09-24  
 13 <160> NUMBER OF SEQ ID NOS: 6  
 15 <170> SOFTWARE: PatentIn version 3.1  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 4753  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Pseudomonas stutzeri  
 22 <220> FEATURE:  
 23 <221> NAME/KEY: CDS  
 24 <222> LOCATION: (1537)..(3603)  
 25 <223> OTHER INFORMATION:  
 28 <400> SEQUENCE: 1

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33	attcggggct	gtccgggtcg	cgcgtgtcg	tgagcggtcg	ccacaggtcg	ctgcgaaacg	180
35	gcggaccgct	ccaaagcgcg	ccgtggatgg	gatcgcccgag	cagtctgtc	agctcccgagg	240
37	aacgttgcga	atgcagcgcg	ccgaggctca	gcccattgcag	atacaggcgc	ggtcggcggtt	300
39	cgcccgccag	ttcggtccag	tagccataga	tctcgccgaa	tagcgccgg	gccacgtcgc	360
41	ggccgtagtc	ggcctccacc	agcagcgccca	gccccgtgtt	cagataggag	tactgcaacg	420
43	ccacgctggc	gatatcgccg	tggtcaggt	attccactgc	tttcatcgcc	gccgggtcga	480
45	tccagccggt	accgggtggc	gtcaccagca	ccagcaccga	tcgctcgaaag	gcgcgcgtgc	540
47	gctcgagctc	gwgcaaggcc	agacgcgcgc	gctggcgccg	ggtctctggc	gcgcgcagac	600
49	cgacgtagac	gcgaaatcgcc	tgcagcgccg	agcggccgct	caagacgtcg	atatcccgccg	660
51	ccgacgggccc	ggagccgatg	aactcgccgc	cggtcgccgc	cagtcctccc	cagcgcagca	720
53	acgaggcccg	gctgcccgtt	ttcagcgccg	aggccggtgg	cgccgtctcc	ggttcgatca	780
55	gggcgtcgta	ctgcgcgaag	gtgcgttcca	gcatgcgcag	tgcggcgccc	gccagcacat	840
57	cgctgagcag	cgaccagaac	agcgccagcg	ccaccagcac	gccgatcact	ttggccaggc	900
59	gccgtggcag	cacgcgtcg	gctgtcccgcc	agacgaagcg	cgacaccagc	cgatacagac	960
61	gcgcgcagcgt	cagcaggatg	agaaaaggctcg	ccagcgccgt	gagaatgact	tcgagcaggt	1020
63	gcgcactgct	caccggcggc	atgcccata	gcccgcgtac	cgcttctgc	cagccggcga	1080
65	cctggctgag	gaaatacccg	gccagcagca	ggcagccgac	cgcgatcagc	agattgaccc	1140
67	gctcgccgt	ccagcctggg	cgctccggca	gttccagata	gcccacagc	cagcggccaga	1200
69	acacgcccag	gccatagccc	accggcagcg	ccgcggccggc	cagcacgc	tggctca	1260
71	tcgagcgccg	cagcaggatg	ggcgtcagcg	ccgcgcagaa	gaacagcggt	cccagcagca	1320
73	ggccgaaacc	ggacagcgag	cgccagatat	agaggacggg	caggtgcagc	atgaagatct	1380
75	ccgcggctgg	gtgacgcgt	cgcgcctcg	catatcgagg	cgtgtccgg	cgtgcgggtc	1440
77	ccgtatggt	ccgcagcagg	ccaatccgat	gcaacatgg	ccgagcggcc	gactcaaacg	1500
79	tctacatttc	cctagtgtcg	ccgaaaccga	tcgccc	atg agc atc	cca gac aac	1554

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81	1			5														
83	acc	tat	atc	gaa	tgg	ctg	gtc	agc	cag	tcc	atg	ctg	cat	gcg	gcc	cgc		1602
84	Thr	Tyr	Ile	Glu	Trp	Leu	Val	Ser	Gln	Ser	Met	Leu	His	Ala	Ala	Arg		
85	10			15			20											
87	gag	cgg	tcg	cgt	cat	tac	gcc	ggc	cag	gcg	cgt	ctc	tgg	cag	cgg	cct		1650
88	Glu	Arg	Ser	Arg	His	Tyr	Ala	Gly	Gln	Ala	Arg	Leu	Trp	Gln	Arg	Pro		
89	25			30			35											
91	tat	gcc	cag	gcc	cgc	ccg	gat	gcc	agc	gcc	atc	gcc	tcg	gtg	tgg		1698	
92	Tyr	Ala	Gln	Ala	Arg	Pro	Arg	Asp	Ala	Ser	Ala	Ile	Ala	Ser	Val	Trp		
93	40			45			50											
95	ttc	acc	gcc	tat	ccg	gcg	gcc	atc	atc	acg	ccg	gaa	ggc	ggc	acg	gta		1746
96	Phe	Thr	Ala	Tyr	Pro	Ala	Ala	Ile	Ile	Thr	Pro	Glu	Gly	Gly	Thr	Val		
97	55			60			65			70								
99	ctc	gag	gcc	ctc	ggc	gac	cgc	ctc	tgg	agt	gcg	ctc	tcc	gaa	ctc		1794	
100	Leu	Glu	Ala	Leu	Gly	Asp	Asp	Arg	Leu	Trp	Ser	Ala	Leu	Ser	Glu	Leu		
101	75			80			85											
103	ggc	gtg	cag	ggc	atc	cac	aac	ggg	ccg	atg	aag	cgt	tcc	ggt	ggc	ctg		1842
104	Gly	Val	Gln	Gly	Ile	His	Asn	Gly	Pro	Met	Lys	Arg	Ser	Gly	Gly	Leu		
105	90			95			100											
107	cgc	gga	cgc	gag	ttc	acc	ccg	acc	atc	gac	ggc	aac	ttc	gac	cgc	atc		1890
108	Arg	Gly	Arg	Gly	Phe	Thr	Pro	Thr	Ile	Asp	Gly	Asn	Phe	Asp	Arg	Ile		
109	105			110			115											
111	agc	ttc	gat	atc	gac	ccg	agc	ctg	ggg	acc	gag	gag	cag	atg	ctg	cag		1938
112	Ser	Phe	Asp	Ile	Asp	Pro	Ser	Leu	Gly	Thr	Glu	Glu	Gln	Met	Leu	Gln		
113	120			125			130											
115	ctc	agc	cg	gtg	gcc	g	cg	ac	aa	cc	atc	gtc	atc	gac	gac	atc		1986
116	Leu	Ser	Arg	Val	Ala	Ala	Ala	His	Asn	Ala	Ile	Val	Ile	Asp	Asp	Ile		
117	135			140			145			150								
119	gtg	ccg	gca	cac	acc	ggc	aag	gg	gtc	gac	ttc	cgc	ctc	g	gaa	atg		2034
120	Val	Pro	Ala	His	Thr	Gly	Lys	Gly	Ala	Asp	Phe	Arg	Leu	Ala	Glu	Met		
121	155			160			165											
123	gcc	tat	ggc	gac	tac	ccc	ggg	ctg	tac	cac	atg	gtg	gaa	atc	cgc	gag		2082
124	Ala	Tyr	Gly	Asp	Tyr	Pro	Gly	Leu	Tyr	His	Met	Val	Glu	Ile	Arg	Glu		
125	170			175			180											
127	gag	gac	tgg	gag	ctg	ctg	ccc	gag	gtg	ccg	ggg	cgt	gat	tcg	gtc		2130	
128	Glu	Asp	Trp	Glu	Leu	Leu	Pro	Glu	Val	Pro	Ala	Gly	Arg	Asp	Ser	Val		
129	185			190			195											
131	aac	ctg	ctg	ccg	ccg	gtg	gtc	gac	ccg	ctc	aag	gaa	aag	cac	tac	atc		2178
132	Asn	Leu	Leu	Pro	Pro	Val	Val	Asp	Arg	Leu	Lys	Glu	Lys	His	Tyr	Ile		
133	200			205			210											
135	gtc	ggc	cag	ctg	cag	ccg	gtg	atc	ttc	tgc	gag	ccg	ggc	atc	aag	gac		2226
136	Val	Gly	Gln	Leu	Gln	Arg	Val	Ile	Phe	Phe	Glu	Pro	Gly	Ile	Lys	Asp		
137	215			220			225			230								
139	acc	gac	tgg	agc	gtc	acc	ggc	gag	gtc	acc	ggg	gtc	gac	ggc	aag	gtg		2274
140	Thr	Asp	Trp	Ser	Val	Thr	Gly	Glu	Val	Thr	Gly	Val	Asp	Gly	Lys	Val		
141	235			240			245											
143	cgt	cgc	tgg	gtc	tat	ctg	cac	tac	ttc	aag	gag	ggc	cag	ccg	tcg	ctg		2322
144	Arg	Arg	Trp	Val	Tyr	Leu	His	Tyr	Phe	Lys	Glu	Gly	Gln	Pro	Ser	Leu		

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147	aac tgg ctc gac ccg acc ttc gcc gcg cag cag ctg atc atc ggc gat			2370
148	Asn Trp Leu Asp Pro Thr Phe Ala Ala Gln Gln Leu Ile Ile Gly Asp			
149	265	270	275	
151	gcg ctg cac gcc atc gac gtc acc ggc gcc cgg gtg ctg cgc ctg gac			2418
152	Ala Leu His Ala Ile Asp Val Thr Gly Ala Arg Val Leu Arg Leu Asp			
153	280	285	290	
155	gcc aac ggc ttc ctc ggc gtc gaa cgg cgc gcc gag ggc acg gcc tgg			2466
156	Ala Asn Gly Phe Leu Gly Val Glu Arg Arg Ala Glu Gly Thr Ala Trp			
157	295	300	305	310
159	tcg gag ggc cac ccg ctg tcc gtc acc ggc aac cag ctg ctc gcc ggg			2514
160	Ser Glu Gly His Pro Leu Ser Val Thr Gly Asn Gln Leu Leu Ala Gly			
161	315	320	325	
163	gcg atc cgc aag gcc ggc ggc ttc agc ttc cag gag ctg aac ctg acc			2562
164	Ala Ile Arg Lys Ala Gly Gly Phe Ser Phe Gln Glu Leu Asn Leu Thr			
165	330	335	340	
167	atc gat gac atc gcc gcc atg tcc cac ggc ggg gcc gat ctg tcc tac			2610
168	Ile Asp Asp Ile Ala Ala Met Ser His Gly Gly Ala Asp Leu Ser Tyr			
169	345	350	355	
171	gac ttc atc acc cgc ccg gcc tat cac cat gcg ttg ctc acc ggc gat			2658
172	Asp Phe Ile Thr Arg Pro Ala Tyr His His Ala Leu Leu Thr Gly Asp			
173	360	365	370	
175	acc gaa ttc ctg cgc atg atg ctg cgc gaa gtc cac gcc ttc ggc atc			2706
176	Thr Glu Phe Leu Arg Met Met Leu Arg Glu Val His Ala Phe Gly Ile			
177	375	380	385	390
179	gac ccg gcg tca ctg atc cat gcg ctg cag aac cat gac gag ttc acc			2754
180	Asp Pro Ala Ser Leu Ile His Ala Leu Gln Asn His Asp Glu Phe Thr			
181	395	400	405	
183	ctg gag ctg gtg cac ttc tgg acg ctg cac gcc tac gac cat tac cac			2802
184	Leu Glu Leu Val His Phe Trp Thr Leu His Ala Tyr Asp His Tyr His			
185	410	415	420	
187	tac aag ggc cag acc ctg ccc ggc ggc cac ctg cgc gaa cat atc cgc			2850
188	Tyr Lys Gly Gln Thr Leu Pro Gly Gly His Leu Arg Glu His Ile Arg			
189	425	430	435	
191	gag gaa atg tac gag cgg ctg acc ggc gaa cac gcg ccg tac aac ctc			2898
192	Glu Glu Met Tyr Glu Arg Leu Thr Gly Glu His Ala Pro Tyr Asn Leu			
193	440	445	450	
195	aag ttc gtc acc aac ggg gtc tcc tgc acc acc gcc agc gtc atc gcc			2946
196	Lys Phe Val Thr Asn Gly Val Ser Cys Thr Thr Ala Ser Val Ile Ala			
197	455	460	465	470
199	gcg gcg ctt aac atc cgt gat ctg gac gcc atc ggc ccg gcc gag gtc			2994
200	Ala Ala Leu Asn Ile Arg Asp Leu Asp Ala Ile Gly Pro Ala Glu Val			
201	475	480	485	
203	gag cag atc cag cgt ctg cat atc ctg ctg gtc atg ttc aat gcc atg			3042
204	Glu Gln Ile Gln Arg Leu His Ile Leu Leu Val Met Phe Asn Ala Met			
205	490	495	500	
207	cag ccc ggc gtc ttc gcc ctc tcc ggc tgg gat ctg gtc ggc gcc ctg			3090
208	Gln Pro Gly Val Phe Ala Leu Ser Gly Trp Asp Leu Val Gly Ala Leu			
209	505	510	515	

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213	520						525				530						
215	ccg	tgg	atc	aat	cgc	ggc	ggc	tat	gac	ctc	gcc	gat	ctg	gcf	ccg	gag	3186
216	Arg	Trp	Ile	Asn	Arg	Gly	Gly	Tyr	Asp	Leu	Ala	Asp	Leu	Ala	Pro	Glu	
217	535						540				545				550		
219	gcf	tcg	gtc	tcc	gcc	gaa	ggc	ctg	ccc	aag	gcc	cgc	tcg	ctg	tac	ggc	3234
220	Ala	Ser	Val	Ser	Ala	Glu	Gly	Leu	Pro	Lys	Ala	Arg	Ser	Leu	Tyr	Gly	
221							555			560				565			
223	agc	ctg	gcc	gag	cag	ctg	cag	cgg	cca	ggc	tcc	ttc	gcc	tgc	cag	ctc	3282
224	Ser	Leu	Ala	Glu	Gln	Leu	Gln	Arg	Pro	Gly	Ser	Phe	Ala	Cys	Gln	Leu	
225							570			575				580			
227	aag	cgc	atc	ctc	agc	gtg	cgc	cag	gcc	tac	gac	atc	gct	gcc	agc	aag	3330
228	Lys	Arg	Ile	Leu	Ser	Val	Arg	Gln	Ala	Tyr	Asp	Ile	Ala	Ala	Ser	Lys	
229							585			590				595			
231	cag	atc	ctg	att	ccg	gat	gtg	cag	gcf	ccg	gga	ctc	ctg	gtg	atg	gtc	3378
232	Gln	Ile	Leu	Ile	Pro	Asp	Val	Gln	Ala	Pro	Gly	Leu	Leu	Val	Met	Val	
233							600			605				610			
235	cac	gag	ctg	cct	gcc	ggc	aag	ggc	gtg	cag	ctc	acg	gca	ctg	aac	ttc	3426
236	His	Glu	Leu	Pro	Ala	Gly	Lys	Gly	Val	Gln	Leu	Thr	Ala	Leu	Asn	Phe	
237							615			620				625		630	
239	agc	gcc	gag	ccg	gtc	agc	gag	acc	atc	tgc	ctg	ccc	ggc	gtg	gcf	ccc	3474
240	Ser	Ala	Glu	Pro	Val	Ser	Glu	Thr	Ile	Cys	Leu	Pro	Gly	Val	Ala	Pro	
241							635			640				645			
243	ggc	ccg	gtg	gtg	gac	atc	att	cac	gag	agt	gtg	gag	ggc	gac	ctc	acc	3522
244	Gly	Pro	Val	Val	Asp	Ile	Ile	His	Glu	Ser	Val	Glu	Gly	Asp	Leu	Thr	
245							650			655				660			
247	gac	aac	tgc	gag	ctg	cag	atc	aac	ctc	gac	ccg	tac	gag	ggg	ctt	gcc	3570
248	Asp	Asn	Cys	Glu	Leu	Gln	Ile	Asn	Leu	Asp	Pro	Tyr	Glu	Gly	Leu	Ala	
249							665			670				675			
251	ctg	cgt	gtg	gtg	agc	gcc	gcf	ccg	ccg	gtg	atc	tgagcgcct	cttcgcgcgc				3623
252	Leu	Arg	Val	Val	Ser	Ala	Ala	Pro	Pro	Val	Ile						
253							680			685							
255	cccggtccg	ccgctatagt	gcf	cag	gcc	ttgggcgcgc	attgcctcg	ccgtcgagac									3683
257	cagcccggt	cgttcaacttc	gttttccgc	cttgcgtgc	tgccgtggc	gctgttgcc											3743
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271	cacgaggagg	atgccccggaa	caacgtcg	ctctggccccc	atgagctcaa	gcacgtcgag											4163
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277	acgcggcgct	gagcgagctg	atcggtgtcg	ctgcccgcac	tgggctgaag	cccaccaatg											4343
279	acgcggcgca	aaacgaaaaaa	ccccgcgcag	gcggggtttc	tgacgcgggt	tgtgcggta											4403
281	gctcagaacg	ccgggaccac	ggcgccttgc	tactttcct	cgatgaactg	cggtacttgc											4463
283	tcgctgtgca	gcf	ccggcagc	cagtttctgc	atggcatacg	tgtcccttgc	gtccggacgg										4523
285	gcgaccagaa	tgttcacgt	tggcgagtc	ctgcccctcg	tcaccaggc	gtcctgggtc											4583

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287 gggttcagct tggcttccag cgcgtagttg gtgttgatca ggcgcaggc gacctgggtc 4643  
 289 agcacgcgcg gcagagtcgc ggcttccagt tcgcggatct tgcatcttctt cgggttctcg 4703  
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 306 20 25 30  
 309 Arg Leu Trp Gln Arg Pro Tyr Ala Gln Ala Arg Pro Arg Asp Ala Ser  
 310 35 40 45  
 313 Ala Ile Ala Ser Val Trp Phe Thr Ala Tyr Pro Ala Ala Ile Thr  
 314 50 55 60  
 317 Pro Glu Gly Gly Thr Val Leu Glu Ala Leu Gly Asp Asp Arg Leu Trp  
 318 65 70 75 80  
 321 Ser Ala Leu Ser Glu Leu Gly Val Gln Gly Ile His Asn Gly Pro Met  
 322 85 90 95  
 325 Lys Arg Ser Gly Gly Leu Arg Gly Arg Glu Phe Thr Pro Thr Ile Asp  
 326 100 105 110  
 329 Gly Asn Phe Asp Arg Ile Ser Phe Asp Ile Asp Pro Ser Leu Gly Thr  
 330 115 120 125  
 333 Glu Glu Gln Met Leu Gln Leu Ser Arg Val Ala Ala Ala His Asn Ala  
 334 130 135 140  
 337 Ile Val Ile Asp Asp Ile Val Pro Ala His Thr Gly Lys Gly Ala Asp  
 338 145 150 155 160  
 341 Phe Arg Leu Ala Glu Met Ala Tyr Gly Asp Tyr Pro Gly Leu Tyr His  
 342 165 170 175  
 345 Met Val Glu Ile Arg Glu Glu Asp Trp Glu Leu Leu Pro Glu Val Pro  
 346 180 185 190  
 349 Ala Gly Arg Asp Ser Val Asn Leu Leu Pro Pro Val Val Asp Arg Leu  
 350 195 200 205  
 353 Lys Glu Lys His Tyr Ile Val Gly Gln Leu Gln Arg Val Ile Phe Phe  
 354 210 215 220  
 357 Glu Pro Gly Ile Lys Asp Thr Asp Trp Ser Val Thr Gly Glu Val Thr  
 358 225 230 235 240  
 361 Gly Val Asp Gly Lys Val Arg Arg Trp Val Tyr Leu His Tyr Phe Lys  
 362 245 250 255  
 365 Glu Gly Gln Pro Ser Leu Asn Trp Leu Asp Pro Thr Phe Ala Ala Gln  
 366 260 265 270  
 369 Gln Leu Ile Ile Gly Asp Ala Leu His Ala Ile Asp Val Thr Gly Ala  
 370 275 280 285  
 373 Arg Val Leu Arg Leu Asp Ala Asn Gly Phe Leu Gly Val Glu Arg Arg  
 374 290 295 300  
 377 Ala Glu Gly Thr Ala Trp Ser Glu Gly His Pro Leu Ser Val Thr Gly  
 378 305 310 315 320  
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**VERIFICATION SUMMARY**

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03052002 15:58:26